

OIPF

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/879,248

DATE: 06/28/2001

TIME: 14:49:27

Input Set : A:\E811.app

Output Set: N:\CRF3\06282001\I879248.raw

**ENTERED**

#2

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3 <110> APPLICANT: Fan, Hao
4 Wei, Zhong-Min
6 <120> TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
7 THEREOF
9 <130> FILE REFERENCE: 21829/81
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/879,248
C--> 12 <141> CURRENT FILING DATE: 2001-06-12
14 <150> PRIOR APPLICATION NUMBER: 60/212,211
15 <151> PRIOR FILING DATE: 2000-06-16
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 338
23 <212> TYPE: PRT
24 <213> ORGANISM: Erwinia chrysanthemi
26 <400> SEQUENCE: 1
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28 1 5 10 15
30 Gly Leu Gly Ala Gln Gly Leu Lys Gly Leu Asn Ser Ala Ala Ser Ser
31 20 25 30
33 Leu Gly Ser Ser Val Asp Lys Leu Ser Ser Thr Ile Asp Lys Leu Thr
34 35 40 45
36 Ser Ala Leu Thr Ser Met Met Phe Gly Gly Ala Leu Ala Gln Gly Leu
37 50 55 60
39 Gly Ala Ser Ser Lys Gly Leu Gly Met Ser Asn Gln Leu Gly Gln Ser
40 65 70 75 80
42 Phe Gly Asn Gly Ala Gln Gly Ala Ser Asn Leu Leu Ser Val Pro Lys
43 85 90 95
45 Ser Gly Gly Asp Ala Leu Ser Lys Met Phe Asp Lys Ala Leu Asp Asp
46 100 105 110
48 Leu Leu Gly His Asp Thr Val Thr Lys Leu Thr Asn Gln Ser Asn Gln
49 115 120 125
51 Leu Ala Asn Ser Met Leu Asn Ala Ser Gln Met Thr Gln Gly Asn Met
52 130 135 140
54 Asn Ala Phe Gly Ser Gly Val Asn Asn Ala Leu Ser Ser Ile Leu Gly
55 145 150 155 160
57 Asn Gly Leu Gly Gln Ser Met Ser Gly Phe Ser Gln Pro Ser Leu Gly
58 165 170 175
60 Ala Gly Gly Leu Gln Gly Leu Ser Gly Ala Gly Ala Phe Asn Gln Leu
61 180 185 190
63 Gly Asn Ala Ile Gly Met Gly Val Gly Gln Asn Ala Ala Leu Ser Ala
64 195 200 205
66 Leu Ser Asn Val Ser Thr His Val Asp Gly Asn Asn Arg His Phe Val
67 210 215 220
69 Asp Lys Glu Asp Arg Gly Met Ala Lys Glu Ile Gly Gln Phe Met Asp
70 225 230 235 240
72 Gln Tyr Pro Glu Ile Phe Gly Lys Pro Glu Tyr Gln Lys Asp Gly Trp

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73          245          250          255
75 Ser Ser Pro Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser Lys
76          260          265          270
78 Pro Asp Asp Asp Gly Met Thr Gly Ala Ser Met Asp Lys Phe Arg Gln
79          275          280          285
81 Ala Met Gly Met Ile Lys Ser Ala Val Ala Gly Asp Thr Gly Asn Thr
82          290          295          300
84 Asn Leu Asn Leu Arg Gly Ala Gly Gly Ala Ser Leu Gly Ile Asp Ala
85 305          310          315          320
87 Ala Val Val Gly Asp Lys Ile Ala Asn Met Ser Leu Gly Lys Leu Ala
88          325          330          335

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90 Asn Ala

94 &lt;210&gt; SEQ ID NO: 2

95 &lt;211&gt; LENGTH: 2141

96 &lt;212&gt; TYPE: DNA

97 <213> ORGANISM: *Erwinia chrysanthemi*

99 &lt;400&gt; SEQUENCE: 2

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101 gcgtttatgg ccgcgatgaa ccggcatcag gcggcgcgct ggtcgcgcga atccggcgctc 120
102 gatctggtat ttcagtttgg ggacaccggg cgtgaactca tgatgcagat tcagccgggg 180
103 cagcaatata ccggcatggt gcgcacgctg ctgcctcgtc gttatcagca ggccggcagag 240
104 tgcgatggct gccatctgtg cctgaacggc agcgatgtat tgatcctctg gtggccgctg 300
105 ccgtcggatc ccggcagtta tccgcaggtg atcgaacggt tgtttgaact ggccgggaatg 360
106 acgttgccgt cgtatccat agcaccgacg gcgcgtccgc agacagggaa cggacgcgcc 420
107 cgatcattaa gataaaggcg gcttttttta ttgcaaacg gtaacggtga ggaaccgttt 480
108 caccgtcggc gtcactcagt aacaagtata catcatgatg cctacatcgg gatcggcgctg 540
109 ggcataccgtt gcagataact ttgcgaacac ctgacatgaa tgaggaaacg aaattatgca 600
110 aattacgata aaagcgcaca tcggcggtga tttggcgctc tccggctctg ggctgggtgc 660
111 tcagggaactg aaaggactga attccgcggc ttcacgctg ggttcacagc tggataaact 720
112 gagcagcacc atcgataagt tgacctccgc gctgacttgc atgatgtttg gcggcgcgct 780
113 ggcgcagggg ctgggcgcga gctcgaagg gctggggatg agcaatcaac tgggccagtc 840
114 tttcggcaat ggcgcgcagg gtgcgagcaa cctgctatcc gtaccgaaat ccggcggcga 900
115 tgcgttgtca aaaatgtttg ataaagcgct ggacgatctg ctgggtcatg acaccgtgac 960
116 caagctgact aaccagagca accaactggc taattcaatg ctgaacgcca gccagatgac 1020
117 ccagggtaat atgaatgcgt tcggcagcgg tgtgaacaac gcactgtcgt ccattctcgg 1080
118 caacggtctc ggccagtcga tgagtggctt ctctcagcct tctctggggg caggcggtt 1140
119 gcagggcctg agcggcgcgg gtgcattcaa ccagttgggt aatgccatcg gcatggcgct 1200
120 ggggcagaat gctgcgctga gtgcgttgag taacgtcagc acccacgtag acggtaaaca 1260
121 ccgccacttt gtagataaag aagatcgcgg catggcgaaa gagatcggcc agtttatgga 1320
122 tcagtatccg gaaatatctg gtaaaccgga ataccagaaa gatggctgga gttcgcgcga 1380
123 gacggacgac aaatcctggg ctaaagcgct gagtaaaccg gatgatgacg gtatgaccgg 1440
124 cgccagcatg gacaaattcc gtcaggcgat gggatgatc aaaagcgcgg tggcggtga 1500
125 taccggcaat accaacctga acctgcgtgg cgcggcggtg gcatcgctgg gtatcgatgc 1560
126 ggctgtcgtc ggcgataaaa tagccaacat gtcgtgggt aagctggcca acgcctgata 1620
127 atctgtgctg gcctgataaa gcggaaacga aaaaagagac ggggaagcct gtctcttttc 1680
128 ttattatgcg gtttatgceg ttacctggac cggttaatca tcgtcatcga tctggtacaa 1740
129 acgcacattt tcccgttcat tcgcgtcgtt acgcgccaca atcgcgatgg catcttctc 1800
130 gtcgctcaga ttgcgcggct gatggggaac gccgggtgga atatagagaa actcgcgggc 1860
131 cagatggaga cagctctgcg ataaatctgt gccgtaacgt gtttctatcc gcccttttag 1920

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132 cagatagatt gcggtttcgt aatcaacatg gtaatgcggt tccgcctgtg cgccggccgg 1980
133 gatcaccaca atattcatag aaagctgtct tgcacctacc gtatcgcggg agataccgac 2040
134 aaaatagggc agtttttgcg tggatatcgt ggggtgttcc ggctgacaa tcttgagttg 2100
135 gttcgtcatc atctttctcc atctgggcga cctgatcgg t 2141
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 403
140 <212> TYPE: PRT
141 <213> ORGANISM: Erwinia amylovora
143 <400> SEQUENCE: 3
144 Met Ser Leu Asn Thr Ser Gly Leu Gly Ala Ser Thr Met Gln Ile Ser
145 1 5 10 15
147 Ile Gly Gly Ala Gly Gly Asn Asn Gly Leu Leu Gly Thr Ser Arg Gln
148 20 25 30
150 Asn Ala Gly Leu Gly Gly Asn Ser Ala Leu Gly Leu Gly Gly Asn
151 35 40 45
153 Gln Asn Asp Thr Val Asn Gln Leu Ala Gly Leu Leu Thr Gly Met Met
154 50 55 60
156 Met Met Met Ser Met Met Gly Gly Gly Gly Leu Met Gly Gly Gly Leu
157 65 70 75 80
159 Gly Gly Gly Leu Gly Asn Gly Leu Gly Gly Ser Gly Gly Leu Gly Glu
160 85 90 95
162 Gly Leu Ser Asn Ala Leu Asn Asp Met Leu Gly Gly Ser Leu Asn Thr
163 100 105 110
165 Leu Gly Ser Lys Gly Gly Asn Asn Thr Thr Ser Thr Thr Asn Ser Pro
166 115 120 125
168 Leu Asp Gln Ala Leu Gly Ile Asn Ser Thr Ser Gln Asn Asp Asp Ser
169 130 135 140
171 Thr Ser Gly Thr Asp Ser Thr Ser Asp Ser Ser Asp Pro Met Gln Gln
172 145 150 155 160
174 Leu Leu Lys Met Phe Ser Glu Ile Met Gln Ser Leu Phe Gly Asp Gly
175 165 170 175
177 Gln Asp Gly Thr Gln Gly Ser Ser Ser Gly Gly Lys Gln Pro Thr Glu
178 180 185 190
180 Gly Glu Gln Asn Ala Tyr Lys Lys Gly Val Thr Asp Ala Leu Ser Gly
181 195 200 205
183 Leu Met Gly Asn Gly Leu Ser Gln Leu Leu Gly Asn Gly Gly Leu Gly
184 210 215 220
186 Gly Gly Gln Gly Gly Asn Ala Gly Thr Gly Leu Asp Gly Ser Ser Leu
187 225 230 235 240
189 Gly Gly Lys Gly Leu Gln Asn Leu Ser Gly Pro Val Asp Tyr Gln Gln
190 245 250 255
192 Leu Gly Asn Ala Val Gly Thr Gly Ile Gly Met Lys Ala Gly Ile Gln
193 260 265 270
195 Ala Leu Asn Asp Ile Gly Thr His Arg His Ser Ser Thr Arg Ser Phe
196 275 280 285
198 Val Asn Lys Gly Asp Arg Ala Met Ala Lys Glu Ile Gly Gln Phe Met
199 290 295 300
201 Asp Gln Tyr Pro Glu Val Phe Gly Lys Pro Gln Tyr Gln Lys Gly Pro
202 305 310 315 320

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204 Gly Gln Glu Val Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser
205           325           330           335
207 Lys Pro Asp Asp Asp Gly Met Thr Pro Ala Ser Met Glu Gln Phe Asn
208           340           345           350
210 Lys Ala Lys Gly Met Ile Lys Arg Pro Met Ala Gly Asp Thr Gly Asn
211           355           360           365
213 Gly Asn Leu Gln Ala Arg Gly Ala Gly Gly Ser Ser Leu Gly Ile Asp
214           370           375           380
216 Ala Met Met Ala Gly Asp Ala Ile Asn Asn Met Ala Leu Gly Lys Leu
217 385           390           395           400
219 Gly Ala Ala
223 <210> SEQ ID NO: 4
224 <211> LENGTH: 1288
225 <212> TYPE: DNA
226 <213> ORGANISM: Erwinia amylovora
228 <400> SEQUENCE: 4
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230 gaggaataacg ttatgagtct gaatacaagt gggctgggag cgtcaacgat gcaaatttct 120
231 atcggcgggtg cgggcggaaa taacgggttg ctgggtacca gtcgccagaa tgctgggttg 180
232 ggtggcaatt ctgcaactgg gctgggcggc ggtaatcaaa atgataccgt caatcagctg 240
233 gctggcttac tcaccggcat gatgatgatg atgagcatga tgggcgggtg tgggctgatg 300
234 ggcgggtggct taggcgggtg cttaggtaat ggcttgggtg gctcagggtg cctgggcgaa 360
235 ggactgtcga acgcgctgaa cgatatgtta ggcggttcgc tgaacacgct gggctcgaaa 420
236 ggcggcaaca ataccacttc aacaacaaat tccccgctgg accaggcgct ggggtattaac 480
237 tcaacgtccc aaaacgacga ttccacctcc ggcacagatt ccacctcaga ctccagcgac 540
238 ccgatgcagc agctgctgaa gatgttcagc gagataatgc aaagcctgtt tggatgatgg 600
239 caagatggca ccagggcgag ttccctctgg ggcaagcagc cgaccgaagg cgagcagaac 660
240 gcctataaaa aaggagtcac tgatgcgctg tcgggcctga tgggtaatgg tctgagccag 720
241 ctcccttgga acgggggact gggaggtggt cagggcggta atgctggcac gggctctgac 780
242 ggttcgtcgc tgggcggcaa agggctgcaa aacctgagcg ggcgggtgga ctaccagcag 840
243 ttaggtaacg ccgtgggtac cggtatcggt atgaaagcgg gcattcaggc gctgaatgat 900
244 atcgggtacg acaggcacag ttcaacctcg tctttcgtca ataaaggcga tcgggcgatg 960
245 gcgaaggaaa tcgggtcagtt catggaccag tatcctgagg tgtttggaac gccgcagtac 1020
246 cagaaaggcc cgggtcagga ggtgaaaacc gatgacaaat catgggcaaa agcactgagc 1080
247 aagccagatg acgacggaat gacaccagcc agtatggagc agttcaacaa agccaagggc 1140
248 atgatcaaaa ggcccatggc ggggtgatacc ggcaacggca acctgcaggc acgcggtgcc 1200
249 ggtggttctt cgtgggttat tgatgccatg atggccgggtg atgccattaa caatatggca 1260
250 cttggcaagc tgggcgcggc ttaagctt 1288
253 <210> SEQ ID NO: 5
254 <211> LENGTH: 1344
255 <212> TYPE: DNA
256 <213> ORGANISM: Erwinia amylovora
258 <400> SEQUENCE: 5
259 atgtcaattc ttacgcttaa caacaatacc tcgtcctcgc cgggtctgtt ccagtcggg 60
260 ggggacaacg ggcttggtgg tcataatgca aattctgcgt tggggcaaca acccatcgat 120
261 cggcaaacca ttgagcaaat ggctcaatta ttggcggaac tgttaaagtc actgctatcg 180
262 ccacaatcag gtaatgcggc aaccggagcc ggtggcaatg accagactac aggagttggt 240
263 aacgctggcg gcctgaacgg acgaaaaggc acagcaggaa ccactccgca gtctgacagt 300
264 cagaacatgc tgagtgaatg gggcaacaac gggctggatc aggccatcac gcccgatggc 360

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265 cagggcggcg ggcagatcgg cgataatcct ttactgaaag ccatgctgaa gcttattgca 420
266 cgcatgatgg acggccaaag cgatcagttt ggccaacctg gtacgggcaa caacagtgcc 480
267 tcttccggta cttcttcata tggcggttcc ccttttaacg atctatcagg ggggaaggcc 540
268 ccttccggca actcccttcc cggaactac tctcccgta gtaccttctc acccccatcc 600
269 acgccaacgt cccctacctc accgcttgat ttcccttctt ctcccaccaa agcagccggg 660
270 ggcagcacgc cggtaacgga tcatcctgac cctgttggtg gcgcgggcat cggggccgga 720
271 aattcggtgg ccttcaccag cgccggcgct aatcagacgg tgctgcatga caccattacc 780
272 gtgaaagcgg gtcagggtgt tgatggcaaa ggacaaacct tcaccgccgg ttcagaatta 840
273 ggcgatggcg gccagtctga aaaccagaaa ccgctgttta tactggaaga cggtgccagc 900
274 ctgaaaaacg tcaccatggg cgacgacggg gcggatggta ttcattctta cggtgatgcc 960
275 aaaatagaca atctgcacgt caccaacgtg ggtgaggacg cgattaccgt taagccaaac 1020
276 agcgcgggca aaaaatccca cgttgaaatc actaacagtt ccttcgagca cgctctgac 1080
277 aagatcctgc agctgaatgc cgatactaac ctgagcggtg acaacgtgaa ggccaaagac 1140
278 tttggtactt ttgtacgcac taacggcggt caacagggtg actgggatct gaatctgac 1200
279 catatcagcg cagaagacgg taagtctctg ttogttaaaa gcgatagcga ggggctaacc 1260
280 gtcaatacca gtgatatctc actgggtgat gttgaaaacc actacaaagt gccgatgtcc 1320
281 gccaacctga aggtggctga atga                                     1344

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284 &lt;210&gt; SEQ ID NO: 6

285 &lt;211&gt; LENGTH: 447

286 &lt;212&gt; TYPE: PRT

287 &lt;213&gt; ORGANISM: Erwinia amylovora

289 &lt;400&gt; SEQUENCE: 6

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290 Met Ser Ile Leu Thr Leu Asn Asn Asn Thr Ser Ser Ser Pro Gly Leu
291   1           5           10           15
293 Phe Gln Ser Gly Gly Asp Asn Gly Leu Gly Gly His Asn Ala Asn Ser
294           20           25           30
296 Ala Leu Gly Gln Gln Pro Ile Asp Arg Gln Thr Ile Glu Gln Met Ala
297           35           40           45
299 Gln Leu Leu Ala Glu Leu Leu Lys Ser Leu Leu Ser Pro Gln Ser Gly
300           50           55           60
302 Asn Ala Ala Thr Gly Ala Gly Gly Asn Asp Gln Thr Thr Gly Val Gly
303           65           70           75           80
305 Asn Ala Gly Gly Leu Asn Gly Arg Lys Gly Thr Ala Gly Thr Thr Pro
306           85           90           95
308 Gln Ser Asp Ser Gln Asn Met Leu Ser Glu Met Gly Asn Asn Gly Leu
309           100          105          110
311 Asp Gln Ala Ile Thr Pro Asp Gly Gln Gly Gly Gly Gln Ile Gly Asp
312           115          120          125
314 Asn Pro Leu Leu Lys Ala Met Leu Lys Leu Ile Ala Arg Met Met Asp
315           130          135          140
317 Gly Gln Ser Asp Gln Phe Gly Gln Pro Gly Thr Gly Asn Asn Ser Ala
318           145          150          155          160
320 Ser Ser Gly Thr Ser Ser Ser Gly Gly Ser Pro Phe Asn Asp Leu Ser
321           165          170          175
323 Gly Gly Lys Ala Pro Ser Gly Asn Ser Pro Ser Gly Asn Tyr Ser Pro
324           180          185          190
326 Val Ser Thr Phe Ser Pro Pro Ser Thr Pro Thr Ser Pro Thr Ser Pro
327           195          200          205
329 Leu Asp Phe Pro Ser Ser Pro Thr Lys Ala Ala Gly Gly Ser Thr Pro

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date